Replacement Sheet

## FIG. 1A

```
Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu Ala Leu Ser His
1               5               10              15

Thr Ala Asn Pro Cys Cys Ser His Pro Cys Gln Asn Arg Gly Val Cys
        20              25              30

Met Ser Val Gly Phe Asp Gln Tyr Lys Cys Asp Cys Thr Arg Thr Gly
        35              40              45

Phe Tyr Gly Glu Asn Cys Ser Thr Pro Glu Phe Leu Thr Arg Ile Lys
    50              55              60

Leu Phe Leu Lys Pro Thr Pro Asn Thr Val His Tyr Ile Leu Thr His
65              70              75              80

Phe Lys Gly Phe Trp Asn Val Val Asn Asn Ile Pro Phe Leu Arg Asn
            85              90              95

Ala Ile Met Ser Tyr Val Leu Thr Ser Arg Ser His Leu Ile Asp Ser
            100             105             110

Pro Pro Thr Tyr Asn Ala Asp Tyr Gly Tyr Lys Ser Trp Glu Ala Phe
        115             120             125

Ser Asn Leu Ser Tyr Tyr Thr Arg Ala Leu Pro Pro Val Pro Asp Asp
    130             135             140

Cys Pro Thr Pro Leu Gly Val Lys Gly Lys Lys Gln Leu Pro Asp Ser
145             150             155             160

Asn Glu Ile Val Glu Lys Leu Leu Leu Arg Arg Lys Phe Ile Pro Asp
            165             170             175

Pro Gln Gly Ser Asn Met Met Phe Ala Phe Phe Ala Gln His Phe Thr
        180             185             190

His Gln Phe Phe Lys Thr Asp His Lys Arg Gly Pro Ala Phe Thr Asn
        195             200             205

Gly Leu Gly His Gly Val Asp Leu Asn His Ile Tyr Gly Glu Thr Leu
    210             215             220

Ala Arg Gln Arg Lys Leu Arg Leu Phe Lys Asp Gly Lys Met Lys Tyr
225             230             235             240

Gln Ile Ile Asp Gly Glu Met Tyr Pro Pro Thr Val Lys Asp Thr Gln
            245             250             255

Ala Glu Met Ile Tyr Pro Pro Gln Val Pro Glu His Leu Arg Phe Ala
            260             265             270

Val Gly Gln Glu Val Phe Gly Leu Val Pro Gly Leu Met Met Tyr Ala
        275             280             285

Thr Ile Trp Leu Arg Glu His Asn Arg Val Cys Asp Val Leu Lys Gln
    290             295             300
```

## FIG 1B

```
Glu His Pro Glu Trp Gly Asp Glu Gln Leu Phe Gln Thr Ser Arg Leu
305         310             315             320

Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Asp Tyr Val Gln
            325             330             335

His Leu Ser Gly Tyr His Phe Lys Leu Lys Phe Asp Pro Glu Leu Leu
            340             345             350

Phe Asn Lys Gln Phe Gln Tyr Gln Asn Arg Ile Ala Ala Glu Phe Asn
        355             360             365

Thr Leu Tyr His Trp His Pro Leu Leu Pro Asp Thr Phe Gln Ile His
    370             375             380

Asp Gln Lys Tyr Asn Tyr Gln Gln Phe Ile Tyr Asn Asn Ser Ile Leu
385             390             395             400

Leu Glu His Gly Ile Thr Gln Phe Val Glu Ser Phe Thr Arg Gln Ile
            405             410             415

Ala Gly Arg Val Ala Gly Gly Arg Asn Val Pro Pro Ala Val Gln Lys
            420             425             430

Val Ser Gln Ala Ser Ile Asp Gln Ser Arg Gln Met Lys Tyr Gln Ser
            435             440             445

Phe Asn Glu Tyr Arg Lys Arg Phe Met Leu Lys Pro Tyr Glu Ser Phe
    450             455             460

Glu Glu Leu Thr Gly Glu Lys Glu Met Ser Ala Glu Leu Glu Ala Leu
465             470             475             480

Tyr Gly Asp Ile Asp Ala Val Glu Leu Tyr Pro Ala Leu Leu Val Glu
            485             490             495

Lys Pro Arg Pro Asp Ala Ile Phe Gly Glu Thr Met Val Glu Val Gly
            500             505             510

Ala Pro Phe Ser Leu Lys Gly Leu Met Gly Asn Val Ile Cys Ser Pro
        515             520             525

Ala Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Gln Ile
    530             535             540

Ile Asn Thr Ala Ser Ile Gln Ser Leu Ile Cys Asn Asn Val Lys Gly
545             550             555             560

Cys Pro Phe Thr Ser Phe Ser Val Pro Asp Pro Glu Leu Ile Lys Thr
            565             570             575

Val Thr Ile Asn Ala Ser Ser Ser Arg Ser Gly Leu Asp Asp Ile Asn
            580             585             590

Pro Thr Val Leu Leu Lys Glu Arg Ser Thr Glu Leu (SEQ ID NO: 10)
            595             600
```

Replacement Sheet

## FIG. 2B

```
CTCAATTCAG TCTCTCATCT GCAATAACGT GAAGGGCTGT CCCTTTACTT CATTCAGTGT 1800
TCCAGATCCA GAGCTCATTA AAACAGTCAC CATCAATGCA AGTTCTTCCC GCTCCGGACT 1860
AGATGATATC AATCCCACAG TACTACTAAA AGAACGGTCG ACTGAACTGT AGAAGTCTAA 1920
TGATCATATT TATTTATTTA TATGAACCAT GTCTATTAAT TTAATTATTT AATAATATTT 1980
ATATTAAACT CCTTATGTTA CTTAACATCT TCTGTAACAG AAGTCAGTAC TCCTGTTGCG 2040
GAGAAAGGAG TCATACTTGT GAAGACTTTT ATGTCACTAC TCTAAAGATT TTGCTGTTGC 2100
TGTTAAGTTT GGAAAACAGT TTTTATTCTG TTTTATAAAC CAGAGAGAAA TGAGTTTTGA 2160
CGTCTTTTTA CTTGAATTTC AACTTATATT ATAAGGACGA AAGTAAAGAT GTTTGAATAC 2220
TTAAACACTA TCACAAGATG CCAAAATGCT GAAAGTTTTT ACACTGTCGA TGTTTCCAAT 2280
GCATCTTCCA TGATGCATTA GAAGTAACTA ATGTTTGAAA TTTTAAAGTA CTTTTGGGTA 2340
TTTTTCTGTC ATCAAACAAA ACAGGTATCA GTGCATTATT AAATGAATAT TTAAATTAGA 2400
CATTACCAGT AATTTCATGT CTACTTTTTA AAATCAGCAA TGAAACAATA ATTTGAAATT 2460
TCTAAATTCA TAGGGTAGAA TCACCTGTAA AAGCTTGTTT GATTCTTAA AGTTATTAAA 2520
CTTGTACATA TACCAAAAAG AAGCTGTCTT GGATTAAAT CTGTAAAATC AGATGAAATT 2580
TTACTACAAT TGCTTGTTAA AATATTTTAT AAGTGATGTT CCTTTTTCAC CAAGAGTATA 2640
AACCTTTTTA GTGTGACTGT TAAAACTTCC TTTTAAATCA AAATGCCAAA TTTATTAAGG 2700
TGGTGGAGCC ACTGCAGTGT TATCTCAAAA TAAGAATATC CTGTTGAGAT ATTCCAGAAT 2760
CTGTTTATAT GGCTGGTAAC ATGTAAAAAC CCCATAACCC CGCCAAAAGG GGTCCTACCC 2820
TTGAACATAA AGCAATAACC AAAGGAGAAA AGCCCAAATT ATTGGTTCCA AATTTAGGGT 2880
TTAAACTTTT TGAAGCAAAC TTTTTTTTAG CCTTGTGCAC TGCAGACCTG GTACTCAGAT 2940
TTTGCTATGA GGTTAATGAA GTACCAAGCT GTGCTTGAAT AACGATATGT TTTCTCAGAT 3000
TTTCTGTTGT ACAGTTTAAT TTAGCAGTCC ATATCACATT GCAAAGTAG CAATGACCTC 3060
ATAAAATACC TCTTCAAAAT GCTTAAATTC ATTTCACACA TTAATTTTAT CTCAGTCTTG 3120
AAGCCAATTC AGTAGGTGCA TTGGAATCAA GCCTGGCTAC CTGCATGCTG TTCCTTTTCT 3180
TTTCTTCTTT TAGCCATTTT GCTAAGAGAC ACAGTCTTCT CAAACACTTC GTTTCTCCTA 3240
TTTTGTTTTA CTAGTTTTAA GATCAGAGTT CACTTTCTTT GGACTCTGCC TATATTTTCT 3300
TACCTGAACT TTTGCAAGTT TTCAGGTAAA CCTCAGCTCA GGACTGCTAT TTAGCTCCTC 3360
TTAAGAAGAT TAAAAAAAAA AAAAAG (SEQ ID NO: 11)                      3387
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